AMENDMENTS TO THE SPECIFICATION

Please amend the specification as follows:

Please delete the following heading and paragraph, beginning at page 1, line 3.

"CROSS REFERENCE TO RELATED APPLICATIONS

This application claims the priority under Title 35 U.S. Code 119(e) from Provisional Application Serial No. 60/413,547 filed Sepetember 25, 2002, which is herein incorporated by reference in its entirety."

Please add the following new paragraph before the paragraph beginning at page 2, line 21:

"The disclosure of U.S. Provisional Application Serial No. 60/413,547 filed 25 Sepetember 2002, is herein incorporated by reference in its entirety."

Please delete the Brief Description of the Drawings and Tables section beginning at page 2, line 24, and insert the following section therefore:

"BRIEF DESCRIPTION OF THE DRAWINGS AND TABLES

Figure 1 shows a ribbon representation of the carbon-alpha trace of the HPTPbeta catalytic domain [SEQ ID NO: 7].

Figure 2 shows the change that occurs in the WPD loop of the HPTPbeta catalytic domain [SEQ ID NO: 7] upon ligand binding (ligand-free structure is shown as darker trace).

Figure 3 shows a superposition between Compound 1 ((S)-[1-Methylcarbamoyl-2-(4-sulfoamino-phenyl)-ethyl]-carbamic acid benzyl ester) (darker) and Compound 2 ({2-(4-Hydroxy-phenyl)-1-[1-methylcarbamoyl-2-(4-sulfoamino-phenyl)-ethylcarbamoyl]-ethyl}-carbamic acid tert-butyl ester) (lighter) structures bound to HPTPbeta catalytic domain [SEQ ID NO: 7].

Figure 4 schematically represents interactions between Compound 1 and the HPTPbeta catalytic domain [SEQ ID NO: 7]: (a) hydrogen bonding and (b) Van der Waals interactions. The ligand is shown in magenta, the main body of the protein is colored blue, and the WPD loop residues are colored red.

Figure 5 shows an overlay of the phosphotyrosine (darker) bound to PTP-1B trap mutant and Compound 1 (lighter) bound to the HPTPbeta catalytic domain [SEQ ID NO: 7].

Figure 6 shows Tyr212 conformation in enzyme complex with Compound 1 (lighter) and Compound 2 (darker).

Figures 7-102 show the atomic structure coordinates for HPTPbeta as derived from a monoclinic crystal of ligand-free HPTPbeta catalytic domain polypeptide.

Figures 103-201 show the atomic structure coordinates for HPTPbeta and the inhibitor molecule as derived from a monoclinic crystal of HPTPbeta bound to the inhibitor Compound 1.

Figures 202-252 show the atomic structure coordinates for HPTPbeta as derived from an orthorhombic crystal of ligand-free HPTPbeta catalytic domain polypeptide.

Figures 253-304 show the atomic structure coordinates for HPTPbeta and the inhibitor molecule as derived from an orthorhombic crystal of HPTPbeta bound to the inhibitor Compound 2."

Please delete the heading beginning at page 15, line 5, and insert the following heading therefore:

"**2. Purification of the catalytic domain of HPTPbeta [SEQ ID NO: 7]**"

Please delete the heading beginning at page 16, line 12, and insert the following heading therefore:

"**3. Crystallization of the catalytic domain of HPTPbeta [SEQ ID NO: 7], collection of X-ray diffraction data, and structure solution**"